AMENDMENTS TO THE CLAIMS

This listing of claims will replace all prior versions and listings of claims in the application:

Listing of Claims:

Claims 1-80 (canceled)

81. (New) A method for analyzing a polynucleotide, comprising:

a) providing a polynucleotide having suspected identity to a defined DNA sequence;

b) using the genetic code to predict the masses of two or more polypeptides encoded in two or more reading frames of said defined DNA sequence, thereby obtaining a predicted peptide mass signature for said defined DNA sequence;

c) expressing two or more fragments from two or more reading frames of said polynucleotide, wherein the reading frames are the same as those used to obtain said predicted peptide mass signature, to create two or more expressed polypeptides;

d) measuring the masses of the two or more expressed polypeptides, thereby obtaining a measured peptide mass signature; and

e) comparing the measured peptide mass signature to the predicted peptide mass signature.

82. (New) The method of claim 81, wherein the polynucleotide contains a difference with respect to the defined DNA sequence and wherein said difference is selected from the group consisting of single nucleotide polymorphism, single nucleotide substitution, single nucleotide deletion, single nucleotide insertion, multiple nucleotide substitution,

multiple nucleotide deletion, multiple nucleotide insertion, DNA duplication, DNA inversion, DNA translocation, and DNA deletion/substitution.

83. (New) The method of claim 81, wherein the polynucleotide comprises an exon.

84. (New) The method of claim 81, wherein the polynucleotide comprises a cDNA.

85. (New) The method of claim 81, wherein the polynucleotide comprises at least one predetermined epitope tag.

86. (New) The method of claim 81, wherein the polypeptides are expressed in a living cell.

87. (New) The method of claim 81, wherein the polypeptides are expressed in a cell free system.

88. (New) The method of claim 87, wherein said cell free system is selected from the group consisting of E. coli extract, rabbit reticulocyte extract, and wheat germ extract.

89. (New) The method of claim 81, further comprising purification of the polypeptide prior to measuring its measured peptide mass signature.

90. (New) The method of claim 89, wherein said purification comprises a method selected from the group consisting of gel electrophoresis, capillary electrophoresis, liquid chromatography (LC), capillary liquid chromatography, high performance liquid chromatography (HPLC), differential centrifugation, filtration, gel filtration, membrane chromatography, affinity purification, biomolecular interaction analysis (BIA), ligand affinity purification, glutathione-S-transferase affinity chromatography, cellulose binding protein affinity chromatography, maltose binding protein affinity chromatography, avidin/streptavidin affinity chromatography, S-tag affinity chromatography, thioredoxin affinity chromatography, metal-chelate affinity chromatography, immobilized metal affinity chromatography, epitope-tag affinity chromatography, immunoaffinity chromatography, immunoaffinity capture, capture using bioreactive mass spectrometer probes, mass spectrometric immunoassay, and immunoprecipitation.

91. (New) The method of claim 90 wherein the polypeptide masses are measured by a method selected from the group consisting of mass spectrometry, MALDI-TOF mass spectrometry, electrospray ionization mass spectrometry (ESI)) tandem mass spectrometry (MS/MS), quadripole time of flight spectrometry (Q-TOF), Fourier transform ion cyclotron resonance (FTICR) mass spectrometry, gel electrophoresis, capillary electrophoresis, and high performance liquid chromatography (HPLC).